

25-90  
0403

#2



OIEPE

## RAW SEQUENCE LISTING

DATE: 11/29/2002

PATENT APPLICATION: US/09/884,319

TIME: 16:01:32

Input Set : N:\CrF3\RULE60\09884319.raw

Output Set: N:\CRF4\11292002\I884319.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
 5 (i) APPLICANT: Lin, Lih-Ling  
 6 Graham, James  
 8 (ii) TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR  
 9 INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND  
 10 BINDING  
 12 (iii) NUMBER OF SEQUENCES: 7  
 14 (iv) CORRESPONDENCE ADDRESS:  
 15 (A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.  
 16 (B) STREET: 87 CambridgePark Drive  
 17 (C) CITY: Cambridge  
 18 (D) STATE: MA  
 19 (E) COUNTRY: USA  
 20 (F) ZIP: 02140  
 22 (v) COMPUTER READABLE FORM:  
 23 (A) MEDIUM TYPE: Floppy disk  
 24 (B) COMPUTER: IBM PC compatible  
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
 28 (vi) CURRENT APPLICATION DATA:  
 C--> 29 (A) APPLICATION NUMBER: US/09/884,319  
 C--> 30 (B) FILING DATE: 18-Jun-2001  
 31 (C) CLASSIFICATION:  
 33 (vii) PRIOR APPLICATION DATA:  
 34 (A) APPLICATION NUMBER: US/09/083,516  
 35 (B) FILING DATE:  
 37 (A) APPLICATION NUMBER: 08/487,942  
 38 (B) FILING DATE:  
 40 (viii) ATTORNEY/AGENT INFORMATION:  
 41 (A) NAME: Brown, Scott A.  
 42 (B) REGISTRATION NUMBER: 32,724  
 43 (C) REFERENCE/DOCKET NUMBER: GI5258  
 45 (ix) TELECOMMUNICATION INFORMATION:  
 46 (A) TELEPHONE: (617) 498-8224  
 47 (B) TELEFAX: (617) 876-5851  
 50 (2) INFORMATION FOR SEQ ID NO: 1:  
 52 (i) SEQUENCE CHARACTERISTICS:  
 53 (A) LENGTH: 1571 base pairs  
 54 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double  
 56 (D) TOPOLOGY: linear  
 58 (ii) MOLECULE TYPE: cDNA

ENTERED

## RAW SEQUENCE LISTING

DATE: 11/29/2002

PATENT APPLICATION: US/09/884,319

TIME: 16:01:32

Input Set : N:\Crif3\RULE60\09884319.raw

Output Set: N:\CRF4\11292002\I884319.raw

```

60      (iii) HYPOTHETICAL: NO
63      (ix) FEATURE:
64          (A) NAME/KEY: CDS
65          (B) LOCATION: 2..529
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 G ATC CCC AGG GTG GAC CTC CGG GTG TGG CAG GAC TGC TGT GAA GAC      46
71   Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp
72     1         5         10         15
74 TGT AGG ACC AGG GGG CAG TTC AAT GCC TTT TCC TAT CAT TTC CGA GGC      94
75 Cys Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly
76     20         25         30
78 AGA CGG TCT CTT GAG TTC AGC TAC CAG GAG GAC AAG CCG ACC AAG AAA      142
79 Arg Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys
80     35         40         45
82 ACA AGA CCA CGG AAA ATA CCC AGT GTT GGG AGA CAG GGG GAA CAT CTC      190
83 Thr Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu
84     50         55         60
86 AGC AAC AGC ACC TCA GCC TTC AGC ACA CGC TCA GAT GCA TCT GGG ACA      238
87 Ser Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr
88     65         70         75
90 AAT GAC TTC AGA GAG TTT GTT CTG GAA ATG CAG AAG ACC ATC ACA GAC      286
91 Asn Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp
92  80         85         90         95
94 CTC AGA ACA CAG ATA AAG AAA CTT GAA TCA CGG CTC AGT ACC ACA GAG      334
95 Leu Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu
96    100        105        110
98 TGC GTG GAT GCC GGG GGC GAA TCT CAC GCC AAC AAC ACC AAG TGG AAA      382
99 Cys Val Asp Ala Gly Gly Glu Ser His Ala Asn Asn Thr Lys Trp Lys
100   115        120        125
102 AAA GAT GCA TGC ACC ATT TGT GAA TGC AAA GAC GGG CAG GTC ACC TGC      430
103 Lys Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys
104   130        135        140
106 TTC GTG GAA GCT TGC CCC CCT GCC ACC TGT GCT GTC CCC GTG AAC ATC      478
107 Phe Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile
108   145        150        155
110 CCA GGG GCC TGC TGT CCA GTC TGC TTA CAG AAG AGG GCG GAG GAA AAG      526
111 Pro Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys
112 160        165        170        175
114 CCC TAGGCTCCTG GGAGGCTCCT CAGAGTTTGT CTGCTGTGCC ATCGTGAGAT      579
115 Pro
118 CGGGTGGCCG ATGGCAGGGA GCTGCGGACT GCAGACCAGG AAACACCCAG AACTCGTGAC      639
120 ATTTTCATGAC AACGTCCAGC TGGTGCTGTT ACAGAAGGCA GTGCAGGAGG CTTCCAACCA      699
122 GAGCATCTGC GGAGAAGGAG GCACAGCAGG TGCCTGAAGG GAAGCAGGCA GGAGTCCTAG      759
124 CTTACGTTA GACTTCTCAG GTTTTTATTT AATTCTTTTA AAATGAAAAA TTGGTGCTAC      819
126 TATTAAATTG CACAGTTGAA TCATTTAGGC GCCTAAATTG ATTTTGCCTC CCAACACCAT      879
128 TTCTTTTTTAA ATAAAGCAGG ATACCTCTAT ATGTCAGCCT TGCCTTGTTT AGATGCCAGG      939
130 AGCCGGCAGA CCTGTCACCC GCAGGTGGGG TGAGTCTCGG AGCTGCCAGA GGGGCTCACC      999
132 GAAATCGGGG TTCCATCACA AGCTATGTTT AAAAAGAAAA TTGGTGTTTG CCAAACGGAA      1059
134 CAGAACCTTT GATGAGAGCG TTCACAGGGA CACTGTCTGG GGGTGCAGTG CAAGCCCCCG      1119

```

## RAW SEQUENCE LISTING

DATE: 11/29/2002

PATENT APPLICATION: US/09/884,319

TIME: 16:01:32

Input Set : N:\Crif3\RULE60\09884319.raw

Output Set: N:\CRF4\11292002\I884319.raw

```

136 GCCTCTTCCC TGGGAACCTC TGAACCTCCTC CTTCTCTGG GCTCTCTGTA ACATTTTACC 1179
138 ACACGTCAGC ATCTAATCCC AAGACAAACA TTCCCGCTGC TCGAAGCAGC TGTATAGCCT 1239
140 GTGACTCTCC GTGTGTCAGC TCCTTCCACA CCTGATTAGA ACATTCATAA GCCACATTTA 1299
142 GAAACAGGTT TGCTTTTCAGC TGTCACCTGC ACACATACTG CCTAGTTGTG AACCAAATGT 1359
144 GAAAAAACCT CCTTCATCCC ATTGTTGTATC TGATACCTGC CGAGGGCCAA GGGTGTGTGT 1419
146 TGACAACGCC GCTCCCAGCC GGCCCTGGTT GCGTCCACGT CCTGAACAAG AGCCGCTTCC 1479
148 GGATGGCTCT TCCCAAGGGA GGAGGAGCTC AAGTGTCTGG AACTGTCTAA CTTCAGGTTG 1539
150 TGTGAGTGCG TAAAAA AAAA AAAA AA 1571

```

153 (2) INFORMATION FOR SEQ ID NO: 2:

155 (i) SEQUENCE CHARACTERISTICS:

156 (A) LENGTH: 176 amino acids

157 (B) TYPE: amino acid

158 (D) TOPOLOGY: linear

160 (ii) MOLECULE TYPE: protein

162 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

164 Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp Cys
165 1 5 10 15
167 Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly Arg
168 20 25 30
170 Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys Thr
171 35 40 45
173 Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu Ser
174 50 55 60
176 Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr Asn
177 65 70 75 80
179 Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp Leu
180 85 90 95
182 Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu Cys
183 100 105 110
185 Val Asp Ala Gly Gly Glu Ser His Ala Asn Asn Thr Lys Trp Lys Lys
186 115 120 125
188 Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys Phe
189 130 135 140
191 Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile Pro
192 145 150 155 160
194 Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys Pro
195 165 170 175

```

198 (2) INFORMATION FOR SEQ ID NO: 3:

200 (i) SEQUENCE CHARACTERISTICS:

201 (A) LENGTH: 1088 base pairs

202 (B) TYPE: nucleic acid

203 (C) STRANDEDNESS: double

204 (D) TOPOLOGY: linear

206 (ii) MOLECULE TYPE: cDNA

208 (iii) HYPOTHETICAL: NO

211 (ix) FEATURE:

212 (A) NAME/KEY: CDS

213 (B) LOCATION: 2..961

216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

## RAW SEQUENCE LISTING

DATE: 11/29/2002

PATENT APPLICATION: US/09/884,319

TIME: 16:01:32

Input Set : N:\Crif3\RULE60\09884319.raw

Output Set: N:\CRF4\11292002\I884319.raw

218	G	AAA	AAA	GGA	GGT	AAA	ACA	GAA	CAG	GAT	GGC	TAT	CAG	AAA	CCC	ACC	46
219	Lys	Lys	Gly	Gly	Lys	Thr	Glu	Gln	Asp	Gly	Tyr	Gln	Lys	Pro	Thr		
220	1				5					10				15			
222	AAC	AAA	CAC	TTC	ACG	CAG	AGT	CCC	AAG	AAG	TCA	GTG	GCC	GAC	CTG	CTG	94
223	Asn	Lys	His	Phe	Thr	Gln	Ser	Pro	Lys	Lys	Ser	Val	Ala	Asp	Leu	Leu	
224				20					25					30			
226	GGG	TCC	TTT	GAA	GGC	AAA	CGA	AGA	CTC	CTT	CTG	ATC	ACT	GCT	CCC	AAG	142
227	Gly	Ser	Phe	Glu	Gly	Lys	Arg	Arg	Leu	Leu	Leu	Ile	Thr	Ala	Pro	Lys	
228				35					40					45			
230	GCT	GAG	AAC	AAT	ATG	TAT	GTG	CAA	CAA	CGT	GAT	GAA	TAT	CTG	GAA	AGT	190
231	Ala	Glu	Asn	Asn	Met	Tyr	Val	Gln	Arg	Asp	Glu	Tyr	Leu	Glu	Ser		
232			50					55					60				
234	TTC	TGC	AAG	ATG	GCT	ACC	AGG	AAA	ATC	TCT	GTG	ATC	ACC	ATC	TTC	GGC	238
235	Phe	Cys	Lys	Met	Ala	Thr	Arg	Lys	Ile	Ser	Val	Ile	Thr	Ile	Phe	Gly	
236		65					70				75						
238	CCT	GTC	AAC	AAC	AGC	ACC	ATG	AAA	ATC	GAC	CAC	TTT	CAG	CTA	GAT	AAT	286
239	Pro	Val	Asn	Asn	Ser	Thr	Met	Lys	Ile	Asp	His	Phe	Gln	Leu	Asp	Asn	
240	80					85				90					95		
242	GAG	AAG	CCC	ATG	CGA	GTG	GTG	GAT	GAT	GAA	GAC	TTG	GTA	GAC	CAG	CGT	334
243	Glu	Lys	Pro	Met	Arg	Val	Val	Asp	Asp	Glu	Asp	Leu	Val	Asp	Gln	Arg	
244				100					105				110				
246	CTC	ATC	AGC	GAG	CTG	AGG	AAA	GAG	TAC	GGA	ATG	ACC	TAC	AAT	GAC	TTC	382
247	Leu	Ile	Ser	Glu	Leu	Arg	Lys	Glu	Tyr	Gly	Met	Thr	Tyr	Asn	Asp	Phe	
248			115						120				125				
250	TTC	ATG	GTG	CTA	ACA	GAT	GTG	GAT	CTG	AGA	GTC	AAG	CAA	TAC	TAT	GAG	430
251	Phe	Met	Val	Leu	Thr	Asp	Val	Asp	Leu	Arg	Val	Lys	Gln	Tyr	Tyr	Glu	
252			130					135					140				
254	GTA	CCA	ATA	ACA	ATG	AAG	TCT	GTG	TTT	GAT	CTG	ATC	GAT	ACT	TTC	CAG	478
255	Val	Pro	Ile	Thr	Met	Lys	Ser	Val	Phe	Asp	Leu	Ile	Asp	Thr	Phe	Gln	
256		145				150					155						
258	TCC	CGA	ATC	AAA	GAT	ATG	GAG	AAG	CAG	AAG	AAG	GAG	GGC	ATT	GTT	TGC	526
259	Ser	Arg	Ile	Lys	Asp	Met	Glu	Lys	Gln	Lys	Lys	Glu	Gly	Ile	Val	Cys	
260	160					165				170					175		
262	AAA	GAG	GAA	GTT	GGG	GGA	GTG	TTA	GAA	CTG	TTC	CCA	ATT	AAT	GGG	AGC	574
263	Lys	Glu	Glu	Val	Gly	Gly	Val	Leu	Glu	Leu	Phe	Pro	Ile	Asn	Gly	Ser	
264				180					185				190				
266	TCT	GTT	GTT	GAG	CGA	GAA	GAC	GTA	CCA	GCC	CAT	TTG	GTG	AAA	GAC	ATT	622
267	Ser	Val	Val	Glu	Arg	Glu	Asp	Val	Pro	Ala	His	Leu	Val	Lys	Asp	Ile	
268			195					200					205				
270	CGT	AAC	TAT	TTT	CAA	GTG	AGC	CCG	GAG	TAC	TTC	TCC	ATG	CTT	CTA	GTC	670
271	Arg	Asn	Tyr	Phe	Gln	Val	Ser	Pro	Glu	Tyr	Phe	Ser	Met	Leu	Leu	Val	
272			210					215					220				
274	GGA	AAA	GAC	GGA	AAT	GTC	AAA	TCC	TGG	TAT	CCT	TCC	CCA	ATG	TGG	TCC	718
275	Gly	Lys	Asp	Gly	Asn	Val	Lys	Ser	Trp	Tyr	Pro	Ser	Pro	Met	Trp	Ser	
276		225				230					235						
278	ATG	GTG	ATT	GTG	TAC	GAT	TTA	ATT	GAT	TCG	ATG	CAA	CTT	CGG	AGA	CAG	766
279	Met	Val	Ile	Val	Tyr	Asp	Leu	Ile	Asp	Ser	Met	Gln	Leu	Arg	Arg	Gln	
280	240					245				250					255		
282	GAA	ATG	GCG	ATT	CAG	CAG	TCA	CTG	GGG	ATG	CGC	TGC	CAG	AAG	ATG	AGT	814

## RAW SEQUENCE LISTING

DATE: 11/29/2002

PATENT APPLICATION: US/09/884,319

TIME: 16:01:32

Input Set : N:\Crif3\RULE60\09884319.raw

Output Set: N:\CRF4\11292002\I884319.raw

```

283 Glu Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser
284                260                265                270
286 ATG CAG GCT ATG GTT ACC ATA GTT ACC ACC AAG GAT ACC AGG ATG GTT      862
287 Met Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val
288                275                280                285
290 ACC AGG ATG ACT ACC GTC ATC ATG AGA GTT ATC ACC ATG GAT ACC CTT      910
291 Thr Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu
292                290                295                300
294 ACT GAG CAG AAA TAT GTA ACC TTA GAC TCA GCC AGT TTC CTC TGC AGC      958
295 Thr Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser
296                305                310                315
298 TGC TAAAACTACA TGTGGCCAGC TCCATTCTTC CACACTGCGT ACTACATTTTC      1011
299 Cys
300 320
302 CTGCCTTTTTT CTTTCAGTGT TTTTCTAAGA CTAAATAAAT AGCAAAC TTT CACCTAAAAA      1071
304 AAAAAAAAAA AAAAAA      1088
307 (2) INFORMATION FOR SEQ ID NO: 4:
309     (i) SEQUENCE CHARACTERISTICS:
310         (A) LENGTH: 320 amino acids
311         (B) TYPE: amino acid
312         (D) TOPOLOGY: linear
314     (ii) MOLECULE TYPE: protein
316     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
318 Lys Lys Gly Gly Lys Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr Asn
319 1      5      10      15
321 Lys His Phe Thr Gln Ser Pro Lys Lys Ser Val Ala Asp Leu Leu Gly
322      20      25      30
324 Ser Phe Glu Gly Lys Arg Arg Leu Leu Ile Thr Ala Pro Lys Ala
325      35      40      45
327 Glu Asn Asn Met Tyr Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser Phe
328      50      55      60
330 Cys Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly Pro
331 65      70      75      80
333 Val Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn Glu
334      85      90      95
336 Lys Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg Leu
337      100     105     110
339 Ile Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe Phe
340      115     120     125
342 Met Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu Val
343      130     135     140
345 Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln Ser
346 145     150     155     160
348 Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys Lys
349      165     170     175
351 Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser Ser
352      180     185     190
354 Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile Arg
355      195     200     205

```

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/884,319

DATE: 11/29/2002

TIME: 16:01:33

Input Set : N:\Crf3\RULE60\09884319.raw

Output Set: N:\CRF4\11292002\I884319.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]